

REMARKS

Entry of the above amendment prior to examination is respectfully requested.

Attached hereto is a marked-up version of the changes made to the specification and claims. The attached pages are captioned "**Version with Markings to Show Changes Made.**"

I. Amendments

The specification has been amended in accordance with 37 C.F.R. §1.821 through 1.825 to add the Sequence Listing.

The specification and claims have been amended in accordance with 37 C.F.R. §1.821(d) to add SEQ ID NO:s.

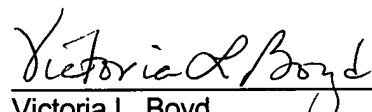
The specification has further been amended to remove embedded hyperlinks in accord with MPEP §608.01.

No new matter is introduced by way of these amendments.

If in the opinion of the Examiner a telephone conference would expedite the prosecution of the subject application, the Examiner is encouraged to call the undersigned at (650) 846-7615.

Respectfully submitted,

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Version with Markings to Show Changes Made

In the specification:

On page 7, please replace the paragraph starting on line 5 with the following:

Figure 2 shows the predicted amino acid sequence (SEQ ID NO:2) and signal sequence (SEQ ID NO:3) based on the nucleotide sequence provided in Figure 1 (SEQ ID NO:1), wherein the signal sequence is indicated as bolded.

On page 19, please replace the paragraph starting on line 3 with the following:

Basic BLASTN search ([<http://www.ncbi.nlm.nih.gov/BLAST>) of the non-redundant nucleic acid sequence database was conducted on September 12, 2001, with the *egl8* gene sequence presented in Figure 1 (SEQ ID NO:1), indicated that the only sequences producing significant alignments (i.e. with an E value of less than 10^{-5}) were GenBank Accession Number S45137 (CMC1, carboxymethylcellulase of *Cryptococcus flavus*).

On page 24, please replace the paragraph starting on line 6 with the following:

Figure 2 shows the predicted amino acid sequence (SEQ ID NO:2) of an exemplary EGVIII polypeptide based on the nucleotide sequence provided in Figure 1 (SEQ ID NO:1). The predicted molecular weight of the encoded EGVIII polypeptide is 46.9kDa. A predicted signal peptide of 19 amino acids precedes the mature amino terminus of EGVIII as provided in the figure suggesting that the EGVIII polypeptide is secreted (Nielsen, H., Engelbrecht, J., Brunak, S., von Heijne, G., Protein Engineering, 10:1-6, 1997). The protein is also predicted to be membrane-anchored via glycosylphosphatidylinositol (Hartmann, T.A. et al., 1989, Proc. Natl. Acad. Sci. USA 86:5786-).

On page 24, please replace the paragraph starting on line 24 with the following:

A Basic BLASTP search ([<http://www.ncbi.nlm.nih.gov/BLAST>) of the non-redundant protein database, conducted on September 12, 2001 with the EGVIII amino acid sequence indicated 52% identity with GenBank Accession Number AB021657 (endoglucanase II of *Trichoderma viride*), 51% sequence identity to GenBank Accession Number M19373 (endoglucanase EG-II precursor of *Trichoderma reesei*), 50% sequence identity to GenBank Accession Number X89564 (endoglucanase 2 of *Penicillium janthinellum*), and 52% sequence identity to GenBank Accession Number U13914 (endo-beta-1,4-glucanase of *Macrophomina*

phaseolina). These sequence similarities indicate that EGVIII is a member of glycosyl hydrolase family 5 (Henrissat, B. and Bairoch, A. (1993) *Biochem. J.* 293:781-788).

On page 29, please replace the paragraph starting on line 1 with the following:

Preferred culture conditions for a given filamentous fungus may be found in the scientific literature and/or from the source of the fungi such as the American Type Culture Collection (ATCC; "[http://]www.atcc.org/"). After fungal growth has been established, the cells are exposed to conditions effective to cause or permit the over expression of EGVIII.

On page 37, please replace the paragraph starting on line 21 with the following:

Exemplary computer programs which can be used to determine identity between two sequences include, but are not limited to, the suite of BLAST programs, e.g., BLASTN, BLASTX, and TBLASTX, BLASTP and TBLASTN, publicly available on the Internet at [http://]www.ncbi.nlm.nih.gov/BLAST/. See also, Altschul, *et al.*, 1990 and Altschul, *et al.*, 1997.

In the claims:

2. An isolated polynucleotide selected from the group consisting of:
 - (a) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGVIII polypeptide having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
 - (b) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGVIII polypeptide having at least 90% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
 - (c) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGVIII polypeptide having at least 95% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
 - (d) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGVIII polypeptide having the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
 - (e) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGVIII polypeptide having at least 95% sequence identity to the amino acid sequence presented as SEQ ID NO:2;

- (f) a nucleic acid sequence which encodes or is complementary to a sequence which encodes an EGVIII polypeptide having the amino acid sequence presented as SEQ ID NO:2;
 - (g) a nucleic acid sequence presented as SEQ ID NO:4, or the complement thereof; and
 - (h) a nucleic acid sequence that hybridizes, under high stringency conditions to the sequence presented as SEQ ID NO:4, or the complement or a fragment thereof, wherein said isolated polynucleotide encodes a polypeptide having the biological activity of an endoglucanase.
8. An expression construct including a polynucleotide sequence (i) having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2), or (ii) being capable of hybridizing to a probe derived from the nucleotide sequence disclosed in Figure 2 (SEQ ID NO:2) under conditions of intermediate to high stringency, or (iii) being complementary to a nucleotide sequence having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2).
18. A substantially purified EGVIII polypeptide with the biological activity of an endoglucanase, comprising a sequence selected from the group consisting of:
- (a) an amino acid sequence having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
 - (b) an amino acid sequence having at least 90% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
 - (c) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
 - (d) an amino acid sequence presented in Figure 2 (SEQ ID NO:2);
 - (e) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented as SEQ ID NO:2;
 - (f) an amino acid sequence presented as SEQ ID NO:2;
 - (g) a substantially purified biologically active fragment of the amino acid sequence presented as SEQ ID NO:2.
25. A detergent composition, said composition comprising a polypeptide selected from the group consisting of:

- (a) an amino acid sequence having at least 85% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
- (b) an amino acid sequence having at least 90% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
- (c) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented in Figure 2 (SEQ ID NO:2);
- (d) an amino acid sequence presented in Figure 2 (SEQ ID NO:2);
- (e) an amino acid sequence having at least 95% sequence identity to the amino acid sequence presented as SEQ ID NO:2;
- (f) an amino acid sequence presented as SEQ ID NO:2;
- (g) a substantially purified biologically active fragment of the amino acid sequence presented as SEQ ID NO:2.